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Use of entomology surveillance data for modeling Culicoides abundance in mainland France

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ABSTRACT

Objective**:** In France, *Culicoides* surveillance was implemented in 2002 in specific areas (Corsica and Mediterranean coastal mainland) and in the whole metropolitan France during 2009-2012 to monitor vectors activity during bluetongue epizootics. The national-scale surveillance was implemented again following the re-emergence in 2015. The purpose of this study was to model the abundance of *Culicoides* using surveillance data.

Materials and methods**:** Since 2016, the *Culicoides* surveillance network operates in 24 eco-climatic zones, with one night trapping per week in one site per eco-climatic zone. Eco-climatic zones were delineated by analyzing the catch data collected in France during 2009-2011, and are homogenous in terms of *Culicoides* abundance, diversity and phenology (start and end of activity period). Minimum and maximum temperature data at each trap location were obtained from Météo France, the French national meteorological service. We applied a specific count model for every eco-climatic zone using a spline transformation of the week number, the minimum and maximum temperature as fixed effects, and the catch site and the year of trapping as random effects. Model fit was evaluated by root mean standard error and mean absolute error.

Result(s)**:** Overall, the model provided a good fit to the data for the 24 eco-climatic zones. They showed that the annual distribution of *Culicoides* varied in terms of abundance, duration, onset and end of activity period, and shape (one or two peaks, with or without plateaus).

Conclusion**:** Although data were collected for surveillance purposes, our modelling approach integrating minimum and maximum temperatures, which are known to be major drivers for *Culicoides* activity, allowed us to predict annual variations in abundance in each zone. Our results may be used to predict at-risk period within each eco-climatic zone and to model bluetongue dynamics and spread in mainland France. This information is essential to define risk-based surveillance programs.

Key words: Culicoides, Abundance modelling, Bluetongue spread, Surveillance and control evaluation

Modelling the Spatial Distribution of the Bluetongue Vector Culicoides brevitarsis in Australia

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ABSTRACT

Objective: Effective decision making in emergency animal disease outbreaks requires an understanding of the potential for disease transmission appropriate for local conditions. Disease models are tools to prepare for such risks. The Australian Animal Disease (AADIS) model has been developed to support foot-and-mouth disease preparedness and response. In this study the capability of AADIS has been extended to simulate the spread of the vector-borne disease bluetongue. The objective of this study was to model the spatial distribution of *Culicoides brevitarsis,* the main competent vector for bluetongue virus in Australia.

Materials and methods: We used a raster approach to adapt Kelso and Milne's 2014 model to estimate the spread of *C. brevitarsis* across Australia as a function of calendar time. Growth and spread of *C. brevitarsis* within each raster cell was dependent on three factors: average daily temperature, short range diffusion and wind-borne dispersal. Wind-borne dispersal was simulated using the Hybrid Single Particle Lagrangian Integrated Trajectory Model. Partial validation of the model was carried out by comparing *C. brevitarsis* counts at locations throughout Australia, as recorded by the National Arbovirus Monitoring Program (NAMP) with the simulated *C. brevitarsis* counts at the same location.

Results: Our model provided biologically plausible estimates of the spatial distribution of *C. brevitarsis* across Australia as a function of time. While *C. brevitarsis* were not present further south than northern coastal New South Wales during the cooler winter months of the year they re-emerged in more southerly coastal regions of New South Wales as temperatures increased and midges were re-introduced from wind-borne spread.

Conclusion: Our model provides a credible estimate of the distribution of *C. brevitarsis* across Australia in response to temperature and wind. This model provides a basis for simulating the dispersion of *C. brevitarsis*, the main vector of bluetongue virus in Australia.

Key words: Models, Vector-borne disease, *Culicoides brevitarsis*, wind spread